



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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171003

STIC-Biotech/ChemLib

From: Hines, Ja-Na  
Sent: Tuesday, November 08, 2005 2:38 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search

Good Afternoon,  
I would like to request a sequence and interference search  
for application 10/043,344. In particular SEQ ID NO:50, 61, 74 and 85.

Thanks so much!!  
Ja-Na Hines (76048)  
AU:1645  
Office: Rem 3B29  
Mailbox: Rem 3C18  
x20859

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: 11/9/05  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# 4  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: [Signature]  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 19:01:45 ; Search time 28.9506 Seconds  
(without alignments)  
116.322 Million cell updates/sec

Title: US-10-043-344-61  
Perfect score: 186  
Sequence: 1 FTSGTLEGGFYGPGEGLGKFLAHDKKVLGVFS 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	92.5	648	2 S70907	transferrin-bindin
2	159	85.5	625	2 D64107	transferrin-bindin
3	159	85.5	630	2 S70909	transferrin-bindin
4	159	85.5	631	2 S70910	transferrin-bindin
5	157	84.4	654	2 S70905	transferrin-bindin
6	156	83.9	631	2 S70908	transferrin-bindin
7	150	80.6	660	2 S70904	transferrin-bindin
8	113.5	61.0	599	2 JN0818	transferrin-bindin
9	109	58.6	547	2 S49814	transferrin-bindin
10	107	57.5	547	2 S49815	transferrin-bindin
11	107	57.5	547	2 A44796	transferrin-bindin
12	102	54.8	593	2 S27483	transferrin-bindin
13	102	54.8	593	2 B44796	transferrin-bindin
14	97	52.2	737	2 H81070	lactoferrin-bindin
15	97	52.2	741	2 D81798	lactoferrin-bindin
16	94.5	50.8	711	2 S70660	transferrin-bindin
17	91.5	49.2	711	2 JN0820	transferrin-bindin
18	91.5	49.2	712	2 E81196	transferrin-bindin
19	90.5	48.7	689	2 S70661	transferrin-bindin
20	90.5	48.7	698	2 D81832	transferrin-bindin
21	78	41.9	289	2 G64105	transferrin-bindin
22	66	35.5	488	2 E81003	transferrin-bindin
23	66	35.5	497	2 C82025	probable periplasm
24	60	32.3	742	2 A49341	isocitrate dehydro
25	59.5	32.0	389	2 T44975	conserved hypotet
26	59	31.7	241	2 AG2915	hypothetical prote
27	59	31.7	241	2 B57690	hypothetical prote
28	56	30.1	394	2 A86431	outer membrane lip
29	55	29.6	200	2 AH3260	

30	54.5	29.3	193	2 H83794	hypothetical prote
31	54.5	29.3	367	2 AF1537	B. subtilis YxjH a
32	54	29.0	1035	2 AD3203	autotransporter pr
33	53.5	28.8	312	2 T37150	probable oxidoredu
34	53.5	28.8	337	2 A69355	adenylosuccinate s
35	53	28.5	265	2 H97349	alpha/beta superfa
36	52.5	28.2	506	1 S34286	pisatin demethylas
37	52.5	28.2	515	1 S45583	pisatin demethylas
38	52.5	28.2	1171	2 T42372	probable guanilate
39	52.5	28.2	1256	2 J50209	brain-specific ang
40	51.5	27.7	367	2 AE1180	B. subtilis YxjH a
41	51.5	27.7	499	2 D72342	tldD protein - The
42	51.5	27.7	707	1 S69781	outer membrane pro
43	51	27.4	148	2 C65068	hypothetical prote
44	51	27.4	163	2 C91092	hypothetical prote
45	51	27.4	163	2 G85937	hypothetical prote

ALIGNMENTS

RESULT 1

S70907  
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB12)  
C:Species: Haemophilus influenzae  
A:Variety: strain SB12  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S70907; S73320  
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.  
Mol. Microbiol. 19, 575-586, 1996  
A>Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes  
A:Reference number: S70901; MUID:96228706; PMID:8830248  
A:Accession: S70907  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-648 <LOC>  
A:Cross-references: UNIPROT:Q48040; EMBL:U15054  
A:Experimental source: strain SB12, clone DS-1047-1-2  
R:Loosmore, S.M.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S73320  
A:Accession: S73320  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-533, 'V', 535-542, 'I', 544-559, 'G', 561-648 <LOW>  
A:Cross-references: EMBL:U15054; NID:g1223946; PIDN:AAC43930.1; PID:g1223947  
A:Experimental source: strain SB12, clone DS-1047-1-2  
C:Genetics:  
A:Gene: tbp2  
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor  
F:i-17/Domain: signal sequence #status predicted <SIG>  
F:i-648/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 92.5%; Score 172; DB 2; Length 648;  
Best Local Similarity 94.3%; Pred. No. 2.1e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTSGTLEGGFYGPGEGLGKFLAHDKKVLGVFS 35  
|||||  
Db 291 FTSGTLEGGFYGPGEGLGKFLAGDKKVLGVFS 325  
|||||

RESULT 2

D64107  
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: D64107  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 456-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,



A:Cross-references: UNIPROT:041168; EMBL:Z46775; NID:g577528; PIDN:CAA86730.1; PID:g57777  
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a





Qy 7 LEGGYPGEQELGGKFLAHDKKVLGVFS 35  
Db 326 LEGGFFGDNGEELAGRFISDINSVFGVFA 354

Search completed: November 9, 2005, 19:24:01  
Job time : 34.9506 secs

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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:42:14 ; Search time 125.914 Seconds  
(without alignments)  
126.074 Million cell updates/sec

Title: US-10-043-344-50

Perfect score: 164

Sequence: 1 LEGFYGPKGELGFRFLAGDKVGVFSK 31

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	89.6	625	1 TBP2_HAEIN	P44971 haemophilus
2	145	88.4	648	2 Q48040	Q48040 haemophilus
3	139	84.8	631	2 Q48041	Q48041 haemophilus
4	135	82.3	630	2 Q48042	Q48042 haemophilus
5	135	82.3	631	2 Q48043	Q48043 haemophilus
6	131	79.9	644	2 Q48034	Q48034 haemophilus
7	131	79.9	654	2 Q48038	Q48038 haemophilus
8	127	77.4	566	2 Q6H804	Q6H804 neisseria m
9	127	77.4	582	2 Q9FC53	Q9FC53 neisseria m
10	127	77.4	593	2 Q6H8W5	Q6H8W5 neisseria c
11	127	77.4	593	2 Q6H8W6	Q6H8W6 neisseria s
12	127	77.4	594	2 Q6H8W3	Q6H8W3 neisseria f
13	127	77.4	602	2 Q53991	Q53991 neisseria m
14	125	76.2	594	2 Q6H8W0	Q6H8W0 neisseria f
15	125	76.2	594	2 Q6H8W1	Q6H8W1 neisseria f
16	125	76.2	660	2 Q57443	Q57443 haemophilus
17	124	75.6	702	2 Q85050	Q85050 moraxella c
18	123	75.0	593	2 Q6H8V1	Q6H8V1 neisseria g
19	123	75.0	593	2 Q6H8W4	Q6H8W4 neisseria f
20	123	75.0	594	2 Q6H8V8	Q6H8V8 neisseria m
21	123	75.0	711	2 Q9ZFD4	Q9ZFD4 moraxella c
22	123	75.0	712	2 Q9Z106	Q9Z106 moraxella c
23	123	75.0	713	2 Q85051	Q85051 moraxella c
24	123	75.0	714	2 Q85056	Q85056 moraxella c
25	119	72.6	681	2 Q9EXC7	Q9EXC7 neisseria m
26	119	72.6	688	2 Q86397	Q86397 neisseria m
27	119	72.6	693	2 Q51285	Q51285 neisseria m
28	119	72.6	693	2 Q9JPL8	Q9JPL8 neisseria m
29	119	72.6	695	2 Q9FCR8	Q9FCR8 neisseria m
30	119	72.6	696	2 Q9EXA7	Q9EXA7 neisseria m
31	119	72.6	696	2 Q9RLM1	Q9RLM1 neisseria m

32	119	72.6	698	2 Q9JPL7	Q9JPL7 neisseria m
33	119	72.6	699	2 Q9EXC4	Q9EXC4 neisseria m
34	119	72.6	711	2 Q51284	Q51284 neisseria m
35	119	72.6	714	2 Q6H8T4	Q6H8T4 neisseria p
36	119	72.6	714	2 Q6H8T5	Q6H8T5 neisseria p
37	119	72.6	715	2 Q9AKU6	Q9AKU6 neisseria m
38	117	71.3	697	2 Q9EXC8	Q9EXC8 neisseria m
39	116	70.7	680	2 Q53990	Q53990 neisseria m
40	116	70.7	705	2 Q51286	Q51286 neisseria m
41	115	70.1	547	2 Q44124	Q44124 actinobacil
42	115	70.1	547	2 Q44168	Q44168 actinobacil
43	115	70.1	547	2 Q44170	Q44170 actinobacil
44	115	70.1	669	2 Q9FCR5	Q9FCR5 neisseria m
45	115	70.1	669	2 Q9FC50	Q9FC50 neisseria m

#### ALIGNMENTS

##### RESULT 1

ID	TBP2_HAEIN	STANDARD;	PRT;	625 AA.
AC	P44971;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Probable transferrin-binding protein 2 precursor.			
GN	Name=tbpB; Synonyms=tbp2; OrderedLocusNames=HI0995;			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Rd / KW20 / ATCC 51907;			
EX	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenny K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,			
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,			
RA	Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae			
RL	Rd.";			
CC	Science 269:496-512(1995).			
CC	-!- FUNCTION: Acts as a transferrin receptor and is required for			
CC	transferrin utilization (by similarity).			
CC	-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid			
CC	anchor (Probable).			

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CC	EMBL; U32780; AAC22657.1; -.
CC	PIR; D64107; D64107.
DR	TIGR; HI0995; -.
DR	InterPro; IPR001677; Transferrin_bind.
DR	Pfam; PF01298; Lipoprotein_5; 1
DR	PROSITE; PS00013; PROXAR_LIPOPROTEIN; 1.
KW	Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor; Signal.
FT	SIGNAL
FT	CHAIN
FT	LIPID
FT	LIPID
FT	Potential.
FT	Probable transferrin-binding protein 2.
FT	N-palmitoyl cysteine (Probable).
FT	S-diacylglycerol cysteine (Probable).

```
SQ SEQUENCE 625 AA; 69031 MW; 52EFBC97B5ED4E9A CRC64;
Query Match      89.6%; Score 147; DB 1; Length 625;
Best Local Similarity 90.3%; Pred. No. 1.3e-11;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEBELGFRFLAGDKKVFVFSK 31
    |||||:||||:||||:||||:||||:||||:
Db 293 LEGGFYGPKEBELGKFLAGDKKVFVFSK 323
    |||||:||||:||||:||||:||||:||||:

RESULT 2
Q48040 ID Q48040 PRELIMINARY; PRT; 648 AA.
AC Q48040;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB12;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15054; AAC43930.1; -.
DR PIR; S70907; S70907.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein 5; 1.
DR SEQUENCE 648 AA; 71246 MW; D89690AE33891A5A CRC64;

Query Match      88.4%; Score 145; DB 2; Length 648;
Best Local Similarity 87.1%; Pred. No. 2.6e-11;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEBELGFRFLAGDKKVFVFSK 31
    |||||:||||:||||:||||:||||:||||:
Db 297 LEGGFYGPKEBELGKFLAGDKKVFVFSK 327
    |||||:||||:||||:||||:||||:||||:

RESULT 3
Q48041 ID Q48041 PRELIMINARY; PRT; 631 AA.
AC Q48041;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB29;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15055; AAC43931.1; -.

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DR PIR; S70908; S70908.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein 5; 1.
SQ SEQUENCE 631 AA; 69770 MW; 8C60777895F3B39 CRC64;

Query Match      84.8%; Score 139; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 1.7e-10;
Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEBELGFRFLAGDKKVFVFSK 31
    |||||:||||:||||:||||:||||:||||:
Db 296 LEGGFYGPKEBELGKFLAGDKKVFVFSK 326
    |||||:||||:||||:||||:||||:||||:

RESULT 4
Q48042 ID Q48042 PRELIMINARY; PRT; 630 AA.
AC Q48042;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB30;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15056; AAC43932.1; -.
DR PIR; S70909; S70909.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein 5; 1.
SQ SEQUENCE 630 AA; 69573 MW; 6FCB2D1B6B642C84 CRC64;

Query Match      82.3%; Score 135; DB 2; Length 630;
Best Local Similarity 83.9%; Pred. No. 6e-10;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEBELGFRFLAGDKKVFVFSK 31
    |||||:||||:||||:||||:||||:||||:
Db 296 LEGGFYGPKEBELGKFLAGDKKVFVFSK 326
    |||||:||||:||||:||||:||||:||||:

RESULT 5
Q48043 ID Q48043 PRELIMINARY; PRT; 631 AA.
AC Q48043;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB32;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,

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RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RL Mol. Microbiol. 19:575-586(1996).
DR EMBL; U15057; AAC43933.1; -.
DR PIR; S70910; S70910.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 631 AA; 70104 MW; E43FF90516F4EDC9 CRC64;

Query Match 82.3%; Score 135; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 6e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 296 LEGGYGNABELGGKFLASDKKVGVSFAK 326

RESULT 6
Q48034
ID Q48034 PRELIMINARY; PRT; 644 AA.
AC Q48034;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbpB;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]_TaxID=727;
RP SEQUENCE FROM N.A.
RC STRAIN=DL63;
RX MEDLINE=95197237; PubMed=7890373;
RA Gray-Owen S.D., Loosmore S., Schryvers A.B.;
RT "Identification and characterization of genes encoding the human
RT transferrin-binding proteins from Haemophilus influenzae.";
RL Infect. Immun. 63:1201-1210(1995).
DR EMBL; U10882; AAA80491.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 644 AA; 70797 MW; 613F9627D8422616 CRC64;

Query Match 79.9%; Score 131; DB 2; Length 644;
Best Local Similarity 80.6%; Pred. No. 2.2e-09;
Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 294 LEGGYGPEGLGGKFLAHDKKVLGVFSFAK 324

RESULT 7
Q48038
ID Q48038 PRELIMINARY; PRT; 654 AA.
AC Q48038;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]_TaxID=727;
RP SEQUENCE FROM N.A.

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RC STRAIN=PAK 12085;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RT Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586(1996).
DR EMBL; U15053; AAC43928.1; -.
DR PIR; S70905; S70905.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 654 AA; 71834 MW; FF3EC728BE5F05A6 CRC64;

Query Match 79.9%; Score 131; DB 2; Length 654;
Best Local Similarity 80.6%; Pred. No. 2.2e-09;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 296 LEGGYGNABELGGKFLANDERKVGVSFAK 326

RESULT 8
Q6H8U4
ID Q6H8U4 PRELIMINARY; PRT; 566 AA.
AC Q6H8U4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Transferrin binding protein B (fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]_TaxID=487;
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha261;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ704752; CAG28834.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 566
SQ SEQUENCE 566 AA; 61751 MW; E0FCA99B682412D8 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 566;
Best Local Similarity 77.4%; Pred. No. 6.8e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 291 LEGGYGPGDELGGKFLANDKKVLAVFSFAK 321

RESULT 9
Q9FCS3
ID Q9FCS3 PRELIMINARY; PRT; 582 AA.
AC Q9FCS3;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Transferrin binding protein B (fragment).
GN Name=tbpB;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RP SEQUENCE FROM N.A.

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=2717;
RX  MEDLINE=20407297; PubMed=10948108;
RA  DOI=10.1128/JAI.68.9.4938-4947.2000;
RA  Rokbi B., Renaud-Mongenie G., Mignon M., Danve B., Poncet D.,
RA  Chabanel C., Caugant D.A., Quentin-Millet M.J.;
RT  "Allelic diversity of the two transferrin binding protein B gene
RT  isotypes among a collection of Neisseria meningitidis strains
RT  representative of serogroup B disease: implication for the composition
RT  of a recombinant TbpB-based vaccine.";
RL  Infect. Immun. 68:4938-4947(2000).
DR  EMBL; AJ279554; CAC05588.1; -.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0004998; F:transferrin receptor activity; IEA.
DR  InterPro; IPR001677; Transferrin_bind.
DR  Pfam; PF01298; Lipoprotein_5; 1.
DR  Name=tbpB;
OS  Neisseria cinerea.
OC  Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC  Neisseriaceae; Neisseria.
OX  NCBI_TaxID=483;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=415;
RA  Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL  Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ704731; CAG28813.2; -.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0004998; F:transferrin receptor activity; IEA.
DR  InterPro; IPR001677; Transferrin_bind.
DR  Pfam; PF01298; Lipoprotein_5; 1.
SQ  SEQUENCE 593 AA; 64218 MW; 8F67EALB15A9FEA9 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 593;
Best Local Similarity 77.4%; Pred. No. 7e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
Db 307 LEGGYGPKGDELGGKFLANDKKVLAVFSK 337

RESULT 10
Q6H8W5
ID Q6H8W5 PRELIMINARY; PRT; 593 AA.
AC Q6H8W5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria cinerea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=483;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=415;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704731; CAG28813.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 593 AA; 64218 MW; 8F67EALB15A9FEA9 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 593;
Best Local Similarity 77.4%; Pred. No. 7e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
Db 318 LEGGYGPKGDELGGKFLANDKKVLAVFSK 348

RESULT 11
Q6H8W6
ID Q6H8W6 PRELIMINARY; PRT; 593 AA.
AC Q6H8W6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

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OS Neisseria sicca.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=490;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9913;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704730; CAG28812.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 593 AA; 64257 MW; 46187C48497275BA CRC64;

Query Match 77.4%; Score 127; DB 2; Length 593;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
Db 318 LEGGYGPKGDELGGKFLANDKKVLAVFSK 348

RESULT 12
Q6H8W3
ID Q6H8W3 PRELIMINARY; PRT; 594 AA.
AC Q6H8W3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria flavescens.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=484;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13120;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704733; CAG28815.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 594 AA; 64390 MW; F096DB9E9B046D0B CRC64;

Query Match 77.4%; Score 127; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
Db 318 LEGGYGPKGDELGGKFLANDKKVLAVFSK 348

RESULT 13
O53991
ID O53991 PRELIMINARY; PRT; 602 AA.
AC O53991;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE TbpB precursor.
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

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OX NCBI_TaxID=484;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3656;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704735; CAG28817.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 594 AA; 64331 MW; 7663C043033D615B CRC64;

Query Match      76.2%; Score 125; DB 2; Length 594;
Best Local Similarity 77.4%; Pred.No.1.3e-08;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 LEGGFYGPQGDELGGKFLAKDKKKVFGVFSNAK 31
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DB     318 LEGGFYGPQGDELGGKFLAKDKKKVLAVFSAK 348

Search completed: November 9, 2005, 19:16:34
Job time : 134.914 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 19:01:45 ; Search time 25.642 Seconds  
(without alignments)  
116.322 Million cell updates/sec

Title: US-10-043-344-50  
Perfect score: 164  
Sequence: 1 LEGGYGPKGRELGRFLAGDKKVGVSFAK 31  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 791\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	89.6	625	2 D64107	transferrin-bindin
2	145	88.4	648	2 S70907	transferrin-bindin
3	139	84.8	631	2 S70908	transferrin-bindin
4	135	82.3	630	2 S70909	transferrin-bindin
5	135	82.3	631	2 S70910	transferrin-bindin
6	131	79.9	654	2 S70905	transferrin-bindin
7	125	76.2	660	2 S70904	transferrin-bindin
8	119	72.6	711	2 S70660	transferrin-bindin
9	115	70.1	547	2 S49815	transferrin-bindin
10	115	70.1	547	2 A44796	transferrin-bindin
11	115	70.1	689	2 S70661	transferrin-bindin
12	115	70.1	698	2 D81832	transferrin-bindin
13	114	69.5	599	2 JN0818	transferrin-bindin
14	111	67.7	711	2 JN0820	transferrin-bindin
15	111	67.7	712	2 E81196	transferrin-bindin
16	105	64.0	547	2 S49814	transferrin-bindin
17	104	63.4	737	2 H81070	lactoferrin-bindin
18	104	63.4	741	2 D81798	lactoferrin-bindin
19	102	62.2	593	2 S27483	transferrin-bindin
20	102	62.2	593	2 B44796	transferrin-bindin
21	66	40.2	488	2 E81003	transferrin-bindin
22	66	40.2	497	2 C82025	probable periplasm
23	62	37.8	289	2 G84105	transferrin-bindin
24	59	36.0	585	2 A83020	probable carbamoyl
25	57	34.8	742	2 A49341	isocitrate dehydro
26	54	32.9	389	2 T44975	dehydrogenase (imp
27	52.5	32.0	521	2 T27606	hypothetical prote
28	52	31.7	316	2 T19435	hypothetical prote
29	52	31.7	539	2 T28770	hypothetical prote

30	52	31.7	675	2 S20819	collagen alpha 3(I
31	51.5	31.4	499	2 D72342	tlcd protein - the
32	51	31.1	320	2 G86400	hypothetical prote
33	51	31.1	413	2 E86400	protein T17H3.4 [i
34	50.5	30.8	137	2 G90214	hypothetical prote
35	50.5	30.8	162	2 A86478	protein F1504.17 [
36	50	30.5	280	2 A42424	chitinase (EC 3.2.
37	50	30.5	374	2 D84632	hypothetical prote
38	49.5	30.2	202	2 E86476	protein F1504.41 [
39	49.5	30.2	202	2 E86347	hypothetical prote
40	49.5	30.2	589	2 AE2504	hypothetical prote
41	49.5	30.2	1690	1 CGHUIB	collagen alpha 4(I
42	49	29.9	483	2 T05088	hypothetical prote
43	48.5	29.6	206	2 T08458	hypothetical prote
44	48	29.3	123	2 A05125	hypothetical prote
45	48	29.3	322	2 S26012	hypothetical prote

ALIGNMENTS

RESULT 1

D64107  
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: D64107  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: D64107  
A;Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A;Residues: 1-625 <TIGR>  
A;Cross-references: UNIPROT:P44971; GB:U32780; GB:L42023; NID:g1574020; PIDN:AAC2657.1;  
C;Genetics:  
A:Gene: tbp2  
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-625/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 89.6%; Score 147; DB 2; Length 625;  
Best Local Similarity 90.3%; Pred. No. 1.1e-12;  
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGRELGRFLAGDKKVGVSFAK 31  
||||| : |||||  
Db 293 LEGGYGPNGBELGKFLAGDKKVGVSFAK 323

RESULT 2

S70907  
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB12)  
C:Species: Haemophilus influenzae  
A:Variety: strain SB12  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S70907; S73320  
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E  
Mol. Microbiol. 19, 575-586, 1996  
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes  
A;Reference number: S70901; MUID:96228706; PMID:8830248  
A;Accession: S70907  
A;Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A;Residues: 1-648 <LOO>  
A;Cross-references: UNIPROT:Q48040; EMBL:U15054  
A;Experimental source: strain SB12, clone DS-1047-1-2  
R;Loosmore, S.M.  
submitted to the EMBL Data Library, September 1994

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A:Reference number: S73320
A:Accession: S73320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533,'V',535-542,'I',544-559,'G',561-648 <LOW>
A:Cross-references: EMBL:U15054; NID:g1223946; PIDN:AAC43930.1; PID:g1223947
A:Experimental source: strain SB12, clone DS-1047-1-2
C:Genetics:
A:Gene: tbp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-648/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match      88.4%; Score 145; DB 2; Length 648;
Best Local Similarity 87.1%; Pred. No. 2.2e-12;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEGGYFGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:|||||:|||||
Db 297 LEGGYFGEGELGKFLAGDKKVGVSFAK 327

RESULT 3
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C:Species: Haemophilus influenzae
A:Variety: strain SB29
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70908; S73321
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70908
A:Molecule type: DNA
A:Residues: 1-631 <LOW>
A:Cross-references: UNIPROT:Q48041; EMBL:U15055
A:Experimental source: strain SB29, clone DS-1090-3-2
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73321
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250,'L',252-349,'RTDATTN',357-631 <LOW>
A:Cross-references: EMBL:U15055; NID:g1223949; PIDN:AAC43931.1; PID:g1223949
A:Experimental source: strain SB29, clone DS-1090-3-2
C:Genetics:
A:Gene: tbp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match      84.8%; Score 139; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 1.5e-11;
Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYFGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:|||||:|||||
Db 296 LEGGYFGNEGELGKFLAGDNRVGVVSFAK 326

RESULT 4
S70909
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB30)
C:Species: Haemophilus influenzae
A:Variety: strain SB30
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70909; S73322
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A:Reference number: S70901; MUID:96228706; PMID:8830248

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A:Accession: S70909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-630 <LOO>
A:Cross-references: UNIPROT:Q48042; EMBL:U15056
A:Experimental source: strain SB30, clone DS-1047-3-3
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73322
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448,'T',450,'I',452-630 <LOW>
A:Cross-references: EMBL:U15056; NID:g1223950; PIDN:AAC43932.1; PID:g1223951
A:Experimental source: strain SB30, clone DS-1047-3-3
C:Genetics:
A:Gene: tbp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-630/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match      82.3%; Score 135; DB 2; Length 630;
Best Local Similarity 83.9%; Pred. No. 5.5e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYFGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:|||||:|||||
Db 296 LEGGYFGNAELGKFLASDKKVGVSFAK 326

RESULT 5
S70910
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB32)
C:Species: Haemophilus influenzae
A:Variety: strain SB32
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70910; S73323
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70910
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-631 <LOO>
A:Cross-references: UNIPROT:Q48043; EMBL:U15057
A:Experimental source: strain SB32, clone DS-1047-4-10
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-241,'P',243-420,'C',422-508,'A',510-631 <LOW>
A:Cross-references: EMBL:U15057; NID:g1223952; PIDN:AAC43933.1; PID:g1223953
A:Experimental source: strain SB32, clone DS-1047-4-10
C:Genetics:
A:Gene: tbp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match      82.3%; Score 135; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 5.5e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYFGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:|||||:|||||
Db 296 LEGGYFGNAELGKFLASDKKVGVSFAK 326

RESULT 6
S70905

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F1-20/Domain: signal sequence #status predicted <SIG>  
F121-711/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 67.7%; Score 111; DB 2; Length 711;  
Best Local Similarity 71.0%; Pred. No. 1.5e-07;  
Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEGGFGPKGELGFRFLAGDKKVFVFSK 31  
DB 335 LSGGFFGQGEELGFRFLSDQKVAVGSAK 365

## RESULT 15

E81196  
transferrin-binding protein 2 NMB0460 [imported] - Neisseria meningitidis (strain MC58 a  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: E81196  
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: E81196  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-712 <TET>  
A:Cross-references: UNIPROT:Q9KOV0; GB:AE002402; GB:AE002098; NID:g7225683; PIDN:AAF4089  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0460  
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match 67.7%; Score 111; DB 2; Length 712;  
Best Local Similarity 71.0%; Pred. No. 1.5e-07;  
Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEGGFGPKGELGFRFLAGDKKVFVFSK 31  
DB 336 LSGGFFGQGEELGFRFLSDQKVAVGSAK 366

Search completed: November 9, 2005, 19:23:55  
Job time : 26.642 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	164	100.0	31	14	US-10-043-344-50	Sequence 50, Appl
2	145	88.4	648	14	US-10-043-344-109	Sequence 109, App
3	139	84.8	631	14	US-10-043-344-111	Sequence 111, App
4	135	82.3	630	14	US-10-043-344-113	Sequence 113, App
5	135	82.3	631	14	US-10-043-344-115	Sequence 115, App
6	131	79.9	644	14	US-10-043-344-6	Sequence 6, Appli
7	131	79.9	654	14	US-10-043-344-12	Sequence 12, Appl
8	125	76.2	365	14	US-10-043-344-156	Sequence 156, App
9	125	76.2	404	14	US-10-043-344-155	Sequence 155, App
10	125	76.2	411	14	US-10-043-344-154	Sequence 154, App
11	125	76.2	417	14	US-10-043-344-153	Sequence 153, App

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RESULT 2
US-10-043-344-109
; Sequence 109, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-109

Query Match      88.4%; Score 145; DB 14; Length 648;
Best Local Similarity 87.1%; Pred. No. 1.1e-12;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:||||:||||:
Db 297 LEGGYGPEGEEELGKFLAGDKKVGVSFAK 327

RESULT 3
US-10-043-344-111
; Sequence 111, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-111

Query Match      84.8%; Score 139; DB 14; Length 631;
Best Local Similarity 83.9%; Pred. No. 8.3e-12;
Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:||||:||||:
Db 296 LEGGYGNGEELGKFLAGDNRRVGVSFAK 326

RESULT 4
US-10-043-344-113
; Sequence 113, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-113

Query Match      82.3%; Score 135; DB 14; Length 630;
Best Local Similarity 83.9%; Pred. No. 3.3e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:||||:||||:
Db 296 LEGGYGNAEELGGKFLASDKKVGVSFAK 326

RESULT 5
US-10-043-344-115
; Sequence 115, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-115

Query Match      82.3%; Score 135; DB 14; Length 631;
Best Local Similarity 83.9%; Pred. No. 3.3e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:||||:||||:
Db 296 LEGGYGNAEELGGKFLASDKKVGVSFAK 326
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; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043.344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-6

Query Match      79.9%; Score 131; DB 14; Length 644;
Best Local Similarity 80.6%; Pred. No. 1.3e-10;
Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 294 LEGGYGPEGQELGKFLANDKVKLVGVSFAK 324

RESULT 7
US-10-043-344-12
; Sequence 12, Application US/10043344
; Publication No. US20030088086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043.344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-12

Query Match      79.9%; Score 131; DB 14; Length 654;
Best Local Similarity 80.6%; Pred. No. 1.3e-10;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGPNABELGKFLANDKVKLVGVSFAK 326

RESULT 8
US-10-043-344-156
; Sequence 156, Application US/10043344
; Publication No. US20030088086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
```

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; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043.344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-156

Query Match      76.2%; Score 125; DB 14; Length 365;
Best Local Similarity 77.4%; Pred. No. 5.5e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 294 LEGGYGPNABELGKFLATDNRVGVFSFAK 324

RESULT 9
US-10-043-344-155
; Sequence 155, Application US/10043344
; Publication No. US20030088086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043.344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-155

Query Match      76.2%; Score 125; DB 14; Length 404;
Best Local Similarity 77.4%; Pred. No. 6.2e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 294 LEGGYGPNABELGKFLATDNRVGVFSFAK 324

RESULT 10
US-10-043-344-154
; Sequence 154, Application US/10043344
; Publication No. US20030088086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
```

```
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-154

Query Match      76.2%; Score 125; DB 14; Length 411;
Best Local Similarity 77.4%; Pred. No. 6.3e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :|||
Db 294 LEGGFYGPNAEELGGKFLATDNRVGVFSAK 324

RESULT 11
US-10-043-344-153
; Sequence 153, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-153

Query Match      76.2%; Score 125; DB 14; Length 417;
Best Local Similarity 77.4%; Pred. No. 6.4e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :|||
Db 294 LEGGFYGPNAEELGGKFLATDNRVGVFSAK 324

RESULT 12
US-10-043-344-152
; Sequence 152, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 152
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-152

Query Match      76.2%; Score 125; DB 14; Length 430;
Best Local Similarity 77.4%; Pred. No. 6.6e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :|||
Db 294 LEGGFYGPNAEELGGKFLATDNRVGVFSAK 324

RESULT 13
US-10-043-344-151
; Sequence 151, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-151

Query Match      76.2%; Score 125; DB 14; Length 463;
Best Local Similarity 77.4%; Pred. No. 7.2e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEELGFRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :|||
Db 294 LEGGFYGPNAEELGGKFLATDNRVGVFSAK 324

RESULT 14
US-10-043-344-150
; Sequence 150, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
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; PRIOR FILING DATE: 1996-05-17  
 ; NUMBER OF SEQ ID NOS: 160  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 150  
 ; LENGTH: 529  
 ; TYPE: PRT  
 ; ORGANISM: Haemophilus influenzae  
 US-10-043-344-150

Query Match 76.2%; Score 125; DB 14; Length 529;  
 Best Local Similarity 77.4%; Pred. No. 8.3e-10;  
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEELGFRFLAGDKKVFVFSK 31  
 Db 294 LEGGFYGNABELGGKFLATDNRVFGVFSK 324

RESULT 15

US-10-043-344-149  
 ; Sequence 149, Application US/10043344  
 ; Publication No. US2003008086A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M.  
 ; APPLICANT: Harkness, Robin E.  
 ; APPLICANT: Schryvers, Anthony B.  
 ; APPLICANT: Chong, Pele  
 ; APPLICANT: Gray-Owen, Scott  
 ; APPLICANT: Murdin, Andrew D.  
 ; APPLICANT: Klein, Michel H.  
 ; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES  
 ; FILE REFERENCE: 1038-1221 MIS  
 ; CURRENT APPLICATION NUMBER: US/10/043.344  
 ; CURRENT FILING DATE: 2002-07-01  
 ; PRIOR APPLICATION NUMBER: 08/649,518  
 ; PRIOR FILING DATE: 1996-05-17  
 ; NUMBER OF SEQ ID NOS: 160  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 149  
 ; LENGTH: 547  
 ; TYPE: PRT  
 ; ORGANISM: Haemophilus influenzae  
 US-10-043-344-149

Query Match 76.2%; Score 125; DB 14; Length 547;  
 Best Local Similarity 77.4%; Pred. No. 8.6e-10;  
 Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGFYGPKEELGFRFLAGDKKVFVFSK 31  
 Db 294 LEGGFYGNABELGGKFLATDNRVFGVFSK 324

Search completed: November 9, 2005, 19:10:50  
 Job time : 133.802 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:42:14 ; Search time 142.16 Seconds  
(without alignments)  
126.074 Million cell updates/sec

Title: US-10-043-344-61

Perfect score: 186

Sequence: 1 FTSGTLEGGYFGPEGQELGKFLAHDKKVLGVFS 35

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	100.0	644	Q48034	haemophilus
2	172	92.5	648	Q48040	haemophilus
3	159	85.5	625	1 TBP2_HAEIN	P44971 haemophilus
4	159	85.5	630	Q48042	haemophilus
5	159	85.5	631	Q48043	haemophilus
6	157	84.4	654	Q48038	haemophilus
7	156	83.9	631	Q48041	haemophilus
8	150	80.6	660	Q57443	haemophilus
9	136.5	73.4	566	Q6804	haemophilus
10	136.5	73.4	582	Q6804	haemophilus
11	136.5	73.4	593	Q6805	neisseria m
12	136.5	73.4	593	Q6805	neisseria c
13	136.5	73.4	593	Q6805	neisseria a
14	136.5	73.4	594	Q6803	neisseria f
15	134.5	72.3	594	Q6804	neisseria m
16	134.5	72.3	594	Q6804	neisseria f
17	132.5	71.2	593	Q6804	neisseria s
18	132.5	71.2	593	Q6804	neisseria f
19	132.5	71.2	594	Q6804	neisseria m
20	124	66.7	713	Q85051	moraxella c
21	121	65.1	702	Q85050	moraxella c
22	118	63.4	711	Q92FD4	moraxella c
23	118	63.4	712	Q92I06	moraxella c
24	118	63.4	714	Q85056	moraxella c
25	115	61.8	706	Q85052	moraxella c
26	115	61.8	709	Q85055	moraxella c
27	114.5	61.6	571	Q6804	neisseria m
28	113.5	61.0	410	Q6804	neisseria m
29	113.5	61.0	567	Q6804	neisseria m
30	113.5	61.0	569	Q6804	neisseria m
31	113.5	61.0	569	Q6804	neisseria m

32	113.5	61.0	570	2	Q6804	neisseria m
33	113.5	61.0	572	2	Q6804	neisseria m
34	113.5	61.0	573	2	Q6804	neisseria m
35	113.5	61.0	579	2	Q6804	neisseria m
36	113.5	61.0	579	2	Q6804	neisseria m
37	113.5	61.0	586	2	Q6804	neisseria m
38	113.5	61.0	599	1	TBB2_NEIMB	Q6804
39	113.5	61.0	599	2	Q6804	neisseria m
40	113.5	61.0	599	2	Q6804	neisseria p
41	113.5	61.0	599	2	Q6804	neisseria p
42	113.5	61.0	599	2	Q6804	neisseria p
43	113.5	61.0	599	2	Q6804	neisseria p
44	113.5	61.0	599	2	Q6804	neisseria m
45	113.5	61.0	605	2	Q6804	neisseria p

## ALIGNMENTS

RESULT 1  
Q48034  
ID Q48034 PRELIMINARY; PRT; 644 AA.  
AC Q48034;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Transferrin binding protein 2.  
GN Name=tbpB;  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellales; Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95197237; PubMed=7890373;  
RA Gray-Owen S.D., Loosmore S., Schryvers A.B.;  
RT "Identification and characterization of genes encoding the human  
transferrin-binding proteins from Haemophilus influenzae.";  
RL Infect. Immun. 63:1201-1210(1995).  
DR EMBL; U10882; AAA80491.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
DR InterPro; IPR001677; Transferrin\_bind.  
DR Pfam; PF01298; Lipoprotein 5; 1.  
SQ SEQUENCE 644 AA; 70797 MW; 613F9627D8422616 CRC64;  
Query Match 100.0%; Score 186; DB 2; Length 644;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FTSGTLEGGYFGPEGQELGKFLAHDKKVLGVFS 35  
Db 288 FTSGTLEGGYFGPEGQELGKFLAHDKKVLGVFS 322  
RESULT 2  
Q48040  
ID Q48040 PRELIMINARY; PRT; 648 AA.  
AC Q48040;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Transferrin binding protein 2.  
GN Name=tbp2;  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellales; Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96228706; PubMed=8830248;

RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,  
 RA Harkness R.E., Pele S.C., Klein M.H.;  
 RT "Cloning and expression of the Haemophilus influenzae transferrin  
 RT receptor genes".  
 RL Mol. Microbiol. 19:575-586(1996).  
 DR EMBL; U15054; AAC43930.1; -.  
 DR PIR; S70907; 625 AA; 71246 MW; D89690AE33891A5A CRC64;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
 DR InterPro; IPR001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 DR SEQUENCE 648 AA; 71246 MW; D89690AE33891A5A CRC64;  
 Query Match 92.5%; Score 172; DB 2; Length 648;  
 Best Local Similarity 94.3%; Pred. No. 9.7e-15;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 35  
 Db 291 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 325  
 RESULT 3  
 TBP2 HAEIN STANDARD; PRT; 625 AA.  
 AC P44971;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Probable transferrin-binding protein 2 precursor.  
 GN Name=tbp2; Synonyms=tbp2; OrderedLocusNames=HI0995;  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Rd / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Karlayne A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.H., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd.";  
 RL Science 269:496-512(1995).  
 CC -1- FUNCTION: Acts as a transferrin receptor and is required for  
 CC transferrin utilization (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid  
 CC anchor (Probable).  
 CC -----  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 CC -----  
 DR EMBL; U32780; AAC22657.1; -.  
 DR PIR; D64107; D64107.  
 DR TIGR; HI0995; -.  
 DR InterPro; IPR001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 KW Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor;  
 KW Signal.  
 FT SIGNAL 1 17 Potential.

FT CHAIN 18 625 Probable transferrin-binding protein 2.  
 FT LIPID 18 18 N-palmitoyl cysteine (Probable).  
 FT LIPID 18 18 S-diacylglycerol cysteine (Probable).  
 SQ SEQUENCE 625 AA; 69031 MW; 52EPEC97B5ED4E9A CRC64;  
 Query Match 85.5%; Score 159; DB 1; Length 625;  
 Best Local Similarity 85.7%; Pred. No. 5.6e-13;  
 Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 35  
 Db 287 FTREGTLEGGFYGPNGEELGGKFLAGDKKVFVFS 321  
 RESULT 4  
 Q48042 PRELIMINARY; PRT; 630 AA.  
 ID Q48042  
 AC Q48042;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Transferrin binding protein 2.  
 GN Name=tbp2;  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SB30;  
 RX MEDLINE=96228706; PubMed=8830248;  
 RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,  
 RA Harkness R.E., Pele S.C., Klein M.H.;  
 RT "Cloning and expression of the Haemophilus influenzae transferrin  
 RT receptor genes".  
 RL Mol. Microbiol. 19:575-586(1996).  
 DR EMBL; U15056; AAC43932.1; -.  
 DR PIR; S70909; S70909.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
 DR InterPro; IPR001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 SQ SEQUENCE 630 AA; 69573 MW; 6FCB2D1B6B642C84 CRC64;  
 Query Match 85.5%; Score 159; DB 2; Length 630;  
 Best Local Similarity 85.7%; Pred. No. 5.6e-13;  
 Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 35  
 Db 290 FTSEGTLEGGFYGPNAEELGGKFLASDKKVFVFS 324  
 RESULT 5  
 Q48043 PRELIMINARY; PRT; 631 AA.  
 ID Q48043  
 AC Q48043;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Transferrin binding protein 2.  
 GN Name=tbp2;  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SB32;  
 RX MEDLINE=96228706; PubMed=8830248;  
 RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,  
 RA Harkness R.E., Pele S.C., Klein M.H.;  
 RT "Cloning and expression of the Haemophilus influenzae transferrin

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RT receptor genes";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15057; AAC43933.1; -.
DR PIR; S70910; S70910.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 631 AA; 70104 MW; B43FF90516F4EDC9 CRC64;

Query Match      85.5%; Score 159; DB 2; Length 631;
Best Local Similarity 85.7%; Pred. No. 5,6e-13;
Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
   |||||
Db 290 FTSEGTLEGGFYGNABELGKFLASDKKVLGVFS 324

RESULT 6
ID Q48038 PRELIMINARY; PRT; 654 AA.
AC Q48038;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=cbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAK 12085;
RX MEDLINE=96228706; PubMed=8830248;
RA Loomore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15053; AAC43928.1; -.
DR PIR; S70905; S70905.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 654 AA; 71834 MW; PF3EC728BE5F05A6 CRC64;

Query Match      84.4%; Score 157; DB 2; Length 654;
Best Local Similarity 82.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
   |||||
Db 290 FTSEGTLEGGFYGNABELGKFLANDEKKVLGVFS 324

RESULT 7
ID Q48041 PRELIMINARY; PRT; 631 AA.
AC Q48041;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=cbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=SB29;
RX MEDLINE=96228706; PubMed=8830248;
RA Loomore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15055; AAC43931.1; -.
DR PIR; S70908; S70908.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 631 AA; 69770 MW; 8C607778953F3B39 CRC64;

Query Match      83.9%; Score 156; DB 2; Length 631;
Best Local Similarity 82.9%; Pred. No. 1.5e-12;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
   |||||
Db 290 FTSEGTLEGGFYGNABELGKFLAGDNRVFGVFS 324

RESULT 8
ID Q57443 PRELIMINARY; PRT; 660 AA.
AC Q57443;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein 2.
GN Name=cbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Minna, and Eagan;
RX MEDLINE=96228706; PubMed=8830248;
RA Loomore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15052; AAC43926.1; -.
DR EMBL; U15051; AAC43924.1; -.
DR PIR; S70904; S70904.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 660 AA; 73069 MW; 87E32401D6BDEP26 CRC64;

Query Match      80.6%; Score 150; DB 2; Length 660;
Best Local Similarity 80.8%; Pred. No. 1e-11;
Matches 28; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
   |||||
Db 288 FTSEGTLEGGFYGNABELGKFLATDNRVFGVFS 322

RESULT 9
ID Q6H8U4 PRELIMINARY; PRT; 566 AA.
AC Q6H8U4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=cbpb;
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OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha261;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704752; CAG28834.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 566
SQ SEQUENCE 566 AA; 61751 MW; 80FCA99B682412D8 CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 566;
Best Local Similarity 75.0%; Pred. No. 6e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 284 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 319

RESULT 10
Q9FCS3
ID Q9FCS3 PRELIMINARY; PRT; 582 AA.
AC Q9FCS3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Namestbpb;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2717;
RX MEDLINE=20407297; PubMed=10948108;
RX DOI=10.1128/IAI.68.9.4938-4947.2000;
RA Rokbi B., Renaud-Mongenie G., Mignon M., Danve B., Poncet D.,
RA Chabanel C., Caugant D.A., Quentin-Willet M.J.;
RT Allelic diversity of the two transferrin binding protein B gene
RT isotypes among a collection of Neisseria meningitidis strains
RT representative of serogroup B disease: implication for the composition
RT of a recombinant TbpB-based vaccine.;
RL Infect. Immun. 68:4938-4947(2000).
DR EMBL; AJ279554; CAC05588.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT CHAIN <1 582 transferrin binding protein B.
SQ SEQUENCE 582 AA; 63426 MW; 26A94AD04F2507F4 CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 582;
Best Local Similarity 75.0%; Pred. No. 6.2e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 300 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 335

RESULT 11
Q6H8W5
ID Q6H8W5 PRELIMINARY; PRT; 593 AA.

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AC Q6H8W5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Namestbpb;
OS Neisseria cinerea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=483;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=415;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704731; CAG28813.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 593 AA; 64218 MW; 8F67EA1B15A9FEA9 CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 593;
Best Local Similarity 75.0%; Pred. No. 6.3e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 311 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 346

RESULT 12
Q6H8W6
ID Q6H8W6 PRELIMINARY; PRT; 593 AA.
AC Q6H8W6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Namestbpb;
OS Neisseria sicca.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=490;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9913;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704730; CAG28812.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 593 AA; 64257 MW; 46187C48497275BA CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 593;
Best Local Similarity 75.0%; Pred. No. 6.3e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 311 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 346

RESULT 13
Q6H8W3
ID Q6H8W3 PRELIMINARY; PRT; 594 AA.
AC Q6H8W3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.

```



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DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria flavescens.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=484;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=414, and 3191;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704736; CAG28818.2; -.
DR EMBL; AJ704734; CAG28816.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein 5; 1.
SQ SEQUENCE 594 AA; 64345 MW; 6200E45E793F20A CRC64;

Query Match 72.3%; Score 134.5; DB 2; Length 594;
Best Local Similarity 75.0%; Pred. No. 1.2e-09;
Matches 27; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 FTSEG-TLEGGFVGPGEQELGGKFLAHDKKVLGVFS 35
   |||:-|||||||:||||||| ||||| |||
Db 311 FVSDSDSLEGGFYGPQDELGGKFLAKDKKVLAVFS 346

Search completed: November 9, 2005, 19:16:34
Job time : 142.16 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:42:14 ; Search time 32.4938 Seconds  
(without alignments)  
126.074 Million cell updates/sec

Title: US-10-043-344-74  
Perfect score: 47  
Sequence: 1 LEGGFYGP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	60	Q6DKQ8	Q6dkq8 neisseria m
2	47	100.0	410	Q6H8U3	Q6h8u3 neisseria m
3	47	100.0	526	Q71R42	Q71r42 haemophilus
4	47	100.0	545	Q71R38	Q71r38 haemophilus
5	47	100.0	547	Q44124	Q44124 actinobacil
6	47	100.0	547	Q44168	Q44168 actinobacil
7	47	100.0	547	Q44170	Q44170 actinobacil
8	47	100.0	560	Q71R40	Q71r40 haemophilus
9	47	100.0	566	Q6H8U4	Q6h8u4 neisseria m
10	47	100.0	567	Q6H8U0	Q6h8u0 neisseria m
11	47	100.0	569	Q6H8T9	Q6h8t9 neisseria m
12	47	100.0	569	Q6H8U2	Q6h8u2 neisseria m
13	47	100.0	570	Q6H8U7	Q6h8u7 neisseria m
14	47	100.0	571	Q6H8U1	Q6h8u1 neisseria m
15	47	100.0	572	Q6H8U6	Q6h8u6 neisseria m
16	47	100.0	573	Q6H8T6	Q6h8t6 neisseria m
17	47	100.0	579	Q6H8T7	Q6h8t7 neisseria m
18	47	100.0	579	Q6PCS1	Q6fcs1 neisseria m
19	47	100.0	582	Q6PCS3	Q6fcs3 neisseria m
20	47	100.0	586	Q6RDV1	Q6rdv1 neisseria m
21	47	100.0	593	Q44169	Q44169 actinobacil
22	47	100.0	593	Q6H8V1	Q6h8v1 neisseria f
23	47	100.0	593	Q6H8W4	Q6h8w4 neisseria f
24	47	100.0	593	Q6H8W5	Q6h8w5 neisseria c
25	47	100.0	593	Q6H8W6	Q6h8w6 neisseria s
26	47	100.0	594	Q6H8V8	Q6h8v8 neisseria m
27	47	100.0	594	Q6H8W0	Q6h8w0 neisseria f
28	47	100.0	594	Q6H8W1	Q6h8w1 neisseria f
29	47	100.0	594	Q6H8W3	Q6h8w3 neisseria f
30	47	100.0	596	Q71R44	Q71r44 actinobacil
31	47	100.0	596	Q83UA7	Q83ua7 actinobacil

32	47	100.0	599	1	TBB2_NEIMB	Q05988 neisseria m
33	47	100.0	599	2	Q6H8V0	Q6h8v0 neisseria l
34	47	100.0	599	2	Q6H8V2	Q6h8v2 neisseria p
35	47	100.0	599	2	Q6H8V4	Q6h8v4 neisseria p
36	47	100.0	599	2	Q6H8V5	Q6h8v5 neisseria p
37	47	100.0	599	2	Q6H8V9	Q6h8v9 neisseria l
38	47	100.0	599	2	Q71US2	Q71us2 neisseria m
39	47	100.0	602	2	OS3991	OS3991 neisseria m
40	47	100.0	603	2	OS3992	OS3992 neisseria m
41	47	100.0	605	2	Q6H8V3	Q6h8v3 neisseria p
42	47	100.0	605	2	Q6H8V6	Q6h8v6 neisseria p
43	47	100.0	625	1	TBP2_HAEIN	P44971 haemophilus
44	47	100.0	630	2	Q48042	Q48042 haemophilus
45	47	100.0	631	2	Q48041	Q48041 haemophilus

ALIGNMENTS

RESULT 1

Q6DKQ8 PRELIMINARY; PRT; 60 AA.  
AC Q6DKQ8; 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DS Transferrin binding protein B (Fragment).  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OX Neisseriaceae; Neisseria.  
CX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Trivedi S.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY680951; AAT71325.1; -  
DR InterPro; IPR001677; Transferrin\_bind.  
DR Pfam; PF01298; Lipoprotein\_5; 1.  
FT NON\_TER 1  
FT NON\_TER 60  
SQ SEQUENCE 60 AA; 6509 MW; 5A7424D75DFADCF4 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0;

Qy 1 LEGGFYGP 8  
Db 52 LEGGFYGP 59  
|||||  
|||||

RESULT 2

Q6H8U3 PRELIMINARY; PRT; 410 AA.  
AC Q6H8U3; 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DS Transferrin binding protein B (Fragment).  
CN Name=tbpB;  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OX Neisseriaceae; Neisseria.  
CX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Alpha3;  
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ704753; CAG28835.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004998; P:transferrin receptor activity; IEA.  
DR InterPro; IPR001677; Transferrin\_bind.

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DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
SQ SEQUENCE 410 AA; 45729 MW; E6CDB0771C99A15B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
|||||
Db 288 LEGGFYGP 295

RESULT 3
Q71R42 PRELIMINARY; PRT; 526 AA.
AC Q71R42;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Haemophilus parasuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=738;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H411;
RA Ladron N., de la Puente V., Ferri E.F.R., Navas J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF376035; AAQ02784.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 526 AA; 57619 MW; A33BE197C9327EE3 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
|||||
Db 271 LEGGFYGP 278

RESULT 4
Q71R38 PRELIMINARY; PRT; 545 AA.
AC Q71R38;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Haemophilus parasuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=738;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H413;
RA de la Puente V., Ladron N., Ferri E.F.R., Navas J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378124; AAQ02788.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 545 AA; 59754 MW; EA12B851A295756D CRC64;

Query Match 100.0%; Score 47; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
|||||
Db 271 LEGGFYGP 278

RESULT 5
Q44124 PRELIMINARY; PRT; 547 AA.
AC Q44124;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbpB;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H49;
RA Gonzalez G.C., Yu R.H., Rostock P.R.Jr., Schryvers A.B.;
RL "Sequence, genetic analysis, and expression of Actinobacillus pleuropneumoniae transferrin receptor genes.";
RL Microbiology 141:2405-2416(1995).
DR EMBL; U16017; AAC43484.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 547 AA; 59818 MW; B8A5D096FBAD088C CRC64;

Query Match 100.0%; Score 47; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
|||||
Db 272 LEGGFYGP 279

RESULT 6
Q44168 PRELIMINARY; PRT; 547 AA.
AC Q44168;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein; transferrin-binding protein.
GN Name=tfbA;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=biotype 2-serotype 2;
RA Bunka S., Potter A., Gerlach G.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z46775; CAA86730.1; -.
DR PIR; S49815; S49815.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 547 AA; 59790 MW; F73734C5A7AC3C56 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
|||||
Db 272 LEGGFYGP 279

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Db      272 LEGGFYGP 279

RESULT 7
Q44170
ID Q44170      PRELIMINARY;      PRT;      547 AA.
AC Q44170
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transferrin-binding protein.
GN Name=tbpA;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serotype 7;
RX MEDLINE=92347999; PubMed=1639494;
RA Gerlach G.F., Klashinsky S., Anderson C., Potter A.A., Wilson P.J.;
RT "Characterization of two genes encoding distinct transferrin-binding
RT proteins in different Actinobacillus pleuropneumoniae isolates.";
RL Infect. Immun. 60:3253-3261(1992).
DR EMBL; M85275; AA21292.1; -.
DR FIR; A44796; A44796.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 547 AA; 59849 MW; C3C870FF5867630F CRC64;

Query Match      100.0%; Score 47; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      272 LEGGFYGP 279

RESULT 8
Q71R40
ID Q71R40      PRELIMINARY;      PRT;      560 AA.
AC Q71R40
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Haemophilus parasuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=738;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H410;
RA Ladrón N., de la Puente V., Ferri E.F.R., Navas J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP376775; RAQ02786.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 560 AA; 61713 MW; 0914C717E6907DC CRC64;

Query Match      100.0%; Score 47; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      288 LEGGFYGP 295

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RESULT 9
Q6H8U4
ID Q6H8U4      PRELIMINARY;      PRT;      566 AA.
AC Q6H8U4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha261;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704752; CAG28834.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 566
SQ SEQUENCE 566 AA; 61751 MW; E0FCA99B682412D8 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      291 LEGGFYGP 298

RESULT 10
Q6H8U0
ID Q6H8U0      PRELIMINARY;      PRT;      567 AA.
AC Q6H8U0
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha563;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704756; CAG28838.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 567
SQ SEQUENCE 567 AA; 61960 MW; 60271A7D3F306892 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      288 LEGGFYGP 295

RESULT 11

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Q6H8T9 PRELIMINARY; PRT; 569 AA.  
 ID Q6H8T9  
 AC Q6H8T9  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Transferrin binding protein B (Fragment).  
 GN Name=tbpB;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Alpha706;  
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ704757; CAG28839.1; -;  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
 DR InterPro; IP001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 DR NON TER 1  
 FT NON TER 569  
 SQ SEQUENCE 569 AA; 62323 MW; F7C31612B9152DEF CRC64;  
 Query Match 100.0%; Score 47; DB 2; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LEGGYFGP 8  
 Db 288 LEGGYFGP 295

RESULT 12  
 Q6H8U2 PRELIMINARY; PRT; 569 AA.  
 ID Q6H8U2  
 AC Q6H8U2  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Transferrin binding protein B (Fragment).  
 GN Name=tbpB;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Alpha306, Alpha749, and Alpha223;  
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ704754; CAG28836.1; -;  
 DR EMBL; AJ704758; CAG28840.1; -;  
 DR EMBL; AJ704751; CAG28833.1; -;  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
 DR InterPro; IP001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 DR NON TER 1  
 FT NON TER 569  
 SQ SEQUENCE 569 AA; 62472 MW; 6AFCB640D99DCA2F CRC64;  
 Query Match 100.0%; Score 47; DB 2; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LEGGYFGP 8  
 Db 288 LEGGYFGP 295

RESULT 13  
 Q6H8U7 PRELIMINARY; PRT; 570 AA.  
 ID Q6H8U7  
 AC Q6H8U7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Transferrin binding protein B (Fragment).  
 GN Name=tbpB;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Alpha122;  
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ704749; CAG28831.1; -;  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
 DR InterPro; IP001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 DR NON TER 1  
 FT NON TER 570  
 SQ SEQUENCE 570 AA; 62724 MW; 622F1F15CACB37C9 CRC64;  
 Query Match 100.0%; Score 47; DB 2; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LEGGYFGP 8  
 Db 288 LEGGYFGP 295

RESULT 14  
 Q6H8U1 PRELIMINARY; PRT; 571 AA.  
 ID Q6H8U1  
 AC Q6H8U1  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Transferrin binding protein B (Fragment).  
 GN Name=tbpB;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Alpha313;  
 RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ704755; CAG28837.1; -;  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
 DR InterPro; IP001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 DR NON TER 1  
 FT NON TER 571  
 SQ SEQUENCE 571 AA; 62265 MW; E3FDEB33921EC2D4 CRC64;  
 Query Match 100.0%; Score 47; DB 2; Length 571;  
 Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LEGGYFGP 8  
 Db 292 LEGGYFGP 299

RESULT 15

Q6H8U6  
ID Q6H8U6 PRELIMINARY; PRT; 572 AA.  
AC Q6H8U6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Transferrin binding protein B (Fragment).  
GN Name=tbpB;  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Alphal7;  
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ704750; CAG28832.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004998; F:transferrin receptor activity; IEA.  
DR InterPro; IPR001677; Transferrin\_bind.  
DR Pfam; PF01298; Lipoprotein\_5; 1.  
FT NON\_TER 1  
FT NON\_TER 572  
SQ SEQUENCE 572 AA; 62540 MW; 049BFPAD043ACBD0A CRC64;  
  
Query Match 100.0%; Score 47; DB 2; Length 572;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LEGFPYGP 8  
Db 292 LEGFPYGP 299  
|||||

Search completed: November 9, 2005, 19:16:35  
Job time : 33.4938 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:43:14 ; Search time 31.6296 Seconds  
(without alignments)  
85.595 Million cell updates/sec

Title: US-10-043-344-85

Perfect score: 40

Sequence: 1 LEGPGYG 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	7	AAR77969	Aar77969 Antigenic
2	40	100.0	7	AAW46162	Aaw46162 Predicted
3	40	100.0	7	AAV51767	Aav51767 H. influe
4	40	100.0	7	AAW54121	Aaw54121 Tbp2 anti
5	40	100.0	7	AAW89426	Aaw89426 Moraxella
6	40	100.0	7	AAV80464	Aav80464 H. influe
7	40	100.0	8	AAR77958	Aar77958 Antigenic
8	40	100.0	8	AAW46151	Aaw46151 Predicted
9	40	100.0	8	AAV51756	Aav51756 H. influe
10	40	100.0	8	AAW54110	Aaw54110 Tbp2 anti
11	40	100.0	8	AAV80453	Aav80453 H. influe
12	40	100.0	15	AAR77974	Aar77974 H. influe
13	40	100.0	15	AAV51789	Aav51789 H. influe
14	40	100.0	15	AAW54133	Aaw54133 Polioviru
15	40	100.0	15	AAV80391	Aav80391 H. influe
16	40	100.0	16	AAR77973	Aar77973 H. influe
17	40	100.0	16	AAV51787	Aav51787 H. influe
18	40	100.0	16	AAV51788	Aav51788 H. influe
19	40	100.0	16	AAW54132	Aaw54132 Polioviru
20	40	100.0	16	AAW54131	Aaw54131 Polioviru
21	40	100.0	16	AAV80390	Aav80390 H. influe
22	40	100.0	16	AAV80389	Aav80389 H. influe
23	40	100.0	17	AAR77971	Aar77971 H. influe
24	40	100.0	17	AAV51786	Aav51786 H. influe
25	40	100.0	17	AAW54130	Aaw54130 Polioviru

ALIGNMENTS

RESULT 1

AAR77969

ID AAR77969 standard; peptide; 7 AA.

XX AAR77969;

XX 09-OCT-1996 (first entry)

XX Antigenic Tbp2 peptide TBP2-36.

XX Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;

KW non-typable strain; Haemophilus influenzae; meningitis.

XX Synthetic.

XX WO9513370-A1.

XX 18-MAY-1995.

XX 07-NOV-1994; 94WO-CA000616.

XX 08-NOV-1993; 93US-00148968.

XX 29-DEC-1993; 93US-00175116.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;

XX Yang Y, Murdin A, Klein M;

XX WPI; 1995-194089/25.

XX Nucleic acids encoding Haemophilus transferrin receptor - used to develop  
prods for detection and in diagnosis, prevention and treatment of  
Haemophilus infection.

XX Claim 11; Page 73; 231pp; English.

XX AAR77933-369 are predicted antigenic peptides derived from conserved  
regions of the Tbp2 protein from H. influenzae strains Egan, Minna, D163  
and non-typable strain PAK12085. The transferrin receptor (TfR) operon  
consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are  
transcribed from a single promoter. H. influenzae TfR is iron- and/or  
haemin-regulated and a putative fur-binding site has been identified  
upstream of tbp2. Antibodies blocking this binding site may prevent  
bacterial growth. Fragments of the TfR (or its genes) are useful in  
CC vaccines to provide protection against, e.g. bacterial meningitis. An  
CC advantage of using the TfR is that it shares homology with TfR of other  
CC H. influenzae strains including non-typable strains. According to the

CC specification the present sequence shows residues 231-238 of Tbp2 from  
 CC the H. influenzae strain Egan  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7  
 |||||  
 Db 1 LEGGFYG 7

RESULT 2  
 AAW46162  
 ID AAW46162 standard; protein; 7 AA.

XX AC AAW46162;

XX 05-MAY-1998 (first entry)

DE Predicted antigenic Tbp1 peptide TBP2-36.

XX Transferrin receptor; Haemophilus influenzae type b; iron;  
 KW human transferrin; iron source; antibody; bacterial growth; vaccine;  
 KW immunogenic truncated analogue; antigen; Tbp1; Tbp2.

XX Synthetic.  
 OS Haemophilus influenzae.

XX WO9640929-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-CA000399.

XX 07-JUN-1995; 95US-00483577.

XX 17-MAY-1996; 96US-00649518.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore SM, Harkness RE, Schryvers AB, Chong P, Gray-Owen S;  
 PI Yang Y, Murdin AD, Klein MH;

XX WPI; 1997-052329/05.

XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used  
 PT to induce protection against disease caused by transferrin producing  
 PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.

XX Example 16; Page 71; 228pp; English.

XX AAW46126-62 are predicted antigenic peptides derived from the Tbp2  
 CC protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin  
 CC receptor, of which Tbp1 is also a subunit. The deduced amino acid  
 CC sequences of Tbp1 and Tbp2 were compared, and regions of conservation  
 CC identified. The above peptides are derived from these regions, the  
 CC present peptide being derived from residues 231-238. Iron is an essential  
 CC nutrient for the growth of these bacteria, and they can utilise human  
 CC transferrin as a source of iron. Antibodies which block the access of the  
 CC transferrin receptor to its iron source prevent bacterial growth. The  
 CC transferrin receptor, or fragments, therefore, are good vaccine  
 CC candidates. An immunogenic composition comprising (or encoding) the  
 CC immunogenic truncated analogue can be used to induce protection against a  
 CC disease caused by a bacterial pathogen that produces the transferrin  
 CC receptor. The immunogenic truncated analogue is also useful as an antigen  
 CC in immunoassays for the detection of Haemophilus transferrin receptor  
 CC antibodies, while the nucleic acid molecule can be used as a  
 CC hybridisation probe for the detection of other transferrin receptor genes

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7  
 |||||  
 Db 1 LEGGFYG 7

RESULT 3  
 AAY51767  
 ID AAY51767 standard; protein; 7 AA.

XX AC AAY51767;

XX 13-JUN-2000 (first entry)

XX H. influenzae antigenic Tbp2 peptide TBP2-36.

XX Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;  
 KW diagnosis.

XX Haemophilus influenzae.

XX US6015688-A.

XX 18-JAN-2000.

XX 07-JUN-1995; 95US-00483577.

XX 08-NOV-1993; 93US-00148968.

XX 29-DEC-1993; 93US-00175116.

XX 08-NOV-1994; 94US-00337483.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;  
 PI Murdin A, Klein M, Chong P;

XX WPI; 1997-052329/05.

XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used  
 PT to induce protection against disease caused by transferrin producing  
 PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.

XX Example 16; Col 39-40; 281pp; English.

XX This invention describes a novel isolated and purified nucleic acid (I)  
 CC encoding an immunogenic, C-terminally truncated analog of one of the  
 CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae  
 CC which has antibacterial activity. (I) are used for recombinant production  
 CC of truncated Tbp; as probes and primers for detecting, and diagnosing  
 CC infection by, Haemophilus, also for isolating similar sequences from  
 CC other bacteria; as immunogens for vaccinating against infections caused  
 CC by bacteria that produce transferrin receptors, e.g. Haemophilus,  
 CC Neisseria or Branhamella. The truncated proteins are useful as immunogens  
 CC (as above); for diagnosing infection (as antigens in immunoassays) and  
 CC for raising antibodies, used for diagnosis of infections or for passive  
 CC immunization. AAY51695-Y51767 represent H. influenzae transferrin  
 CC receptor proteins Tbp1 and Tbp2 antigenic peptide fragments

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7  
 |||||  
 Db 1 LEGGFYG 7

RESULT 4

```

AAW54121
ID AAW54121 standard; peptide; 7 AA.
XX
XX AC AAW54121;
XX
XX DT 20-JUN-1998 (first entry)
XX
XX DE Tbp2 antigenic peptide TBP2-36.
XX
XX KW tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
XX KW passive immunisation; transferrin receptor operon.
XX OS Haemophilus influenzae.
XX
XX PN US5708149-A.
XX
XX PD 13-JAN-1998.
XX
XX PF 07-JUN-1995; 95US-00487890.
XX
XX PR 08-NOV-1993; 93US-00148968.
XX PR 29-DEC-1993; 93US-00175116.
XX PR 08-NOV-1994; 94US-00337483.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX
XX PI Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;
XX PI Murdin A, Schryvers A;
XX
XX DR WPI; 1998-100410/09.
XX
XX PT Purification of recombinant Haemophilus transferrin-binding protein - by
XX PT solubilising inclusion bodies separated from cell lysate.
XX
XX PS Example 16/17; Column 37-38; 261pp; English.
XX
XX CC Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from
XX CC the Tbp2 protein. The Tbp2 protein is one of two proteins with genes
XX CC found on the transferrin operon. These peptides can be used along with
XX CC the genes, DNA sequences and recombinant proteins for diagnosis,
XX CC immunisation and the generation of diagnostic and immunological reagents.
XX CC They can also be used to protect from bacteria that produce transferrin
XX CC receptor protein
XX
XX SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 40; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFGY 7
XX Db 1 LEGGFGY 7
XX
XX RESULT 5
XX AAW89426
XX ID AAW89426 standard; peptide; 7 AA.
XX
XX AC AAW89426;
XX
XX DT 21-JUN-1999 (first entry)
XX
XX DE Moraxella lactoferrin binding protein 2 (Lbp2) epitope.
XX
XX KW Lactoferrin receptor; lactoferrin binding protein; Lbp1; lbpA gene;
XX KW infection; otitis media; sinusitis; conjunctivitis; pneumonia;
XX KW bronchitis; tracheitis; emphysema; diagnosis; therapy; vaccine;
XX KW Branhamella catarrhalis; epitope.
XX
XX OS Moraxella catarrhalis.
XX
XX PN W09855606-A2.
XX
XX Query Match 100.0%; Score 40; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFGY 7
XX Db 1 LEGGFGY 7
XX
XX RESULT 5
XX AAW89426
XX ID AAW89426 standard; peptide; 7 AA.
XX
XX AC AAW89426;
XX
XX DT 21-JUN-1999 (first entry)
XX
XX DE Moraxella lactoferrin binding protein 2 (Lbp2) epitope.
XX
XX KW Lactoferrin receptor; lactoferrin binding protein; Lbp1; lbpA gene;
XX KW infection; otitis media; sinusitis; conjunctivitis; pneumonia;
XX KW bronchitis; tracheitis; emphysema; diagnosis; therapy; vaccine;
XX KW Branhamella catarrhalis; epitope.
XX
XX OS Moraxella catarrhalis.
XX
XX PN W09855606-A2.
XX
XX Query Match 100.0%; Score 40; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFGY 7
XX Db 1 LEGGFGY 7
XX
XX RESULT 6
XX AAY80464
XX ID AAY80464 standard; peptide; 7 AA.
XX
XX AC AAY80464;
XX
XX DT 06-JUN-2000 (first entry)
XX
XX DE H. influenzae transferrin receptor Tbp1 epitope TBP2-36.
XX
XX KW Antibacterial; antiinflammatory; auditory; respiratory; antibody;
XX KW antiserum; transferrin receptor; immunogen; epitope; otitis media;
XX KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
XX
XX OS Haemophilus influenzae.
XX
XX PN US6008326-A.
XX
XX PD 28-DEC-1999.
XX
XX PF 07-JUN-1995; 95US-00474671.
XX
XX PR 08-NOV-1993; 93US-00148968.
XX PR 29-DEC-1993; 93US-00175116.
XX PR 08-NOV-1995; 95US-00337483.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX
XX PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
XX PI Murdin A, Schryvers A;
XX
XX DR WPI; 2000-096387/08.
XX
XX PT Antibodies specific for transferrin receptor proteins of Haemophilus

```

PT influenzae, useful for treating otitis media, epiglottitis, pneumonia and  
 XX tracheobronchitis.

PS Disclosure; Col 39-40; 252pp; English.

CC The invention relates to novel antibodies (or monospecific antisera)  
 CC specific for single transferrin receptor proteins (or immunogenic  
 CC fragment) from strains of Haemophilus influenzae. This sequence  
 CC corresponds to an epitope from the H. influenzae transferrin receptor  
 CC protein Tbp2. The antibodies may be used for preventing and treating  
 CC infections and disorders caused by H. influenzae, including bacterial  
 CC meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis.  
 CC The antibodies may also be used to detect the presence of H. influenzae  
 CC proteins in samples according to standard methodologies (e.g. enzyme  
 CC linked immunosorbant assay (ELISA)) and hence diagnose infections  
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7  
 Db 1 LEGGFYG 7

RESULT 7

AAR77958  
 ID AAR77958 standard; peptide; 8 AA.

AC AAR77958;

DT 09-OCT-1996 (first entry)

XX Antigenic Tbp2 peptide TBP2-25.

XX Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;  
 KW non-typable strain; Haemophilus influenzae; meningitis.

OS Synthetic.

XX WO9513370-A1.

XX 18-MAY-1995.

XX 07-NOV-1994; 94WO-CA000616.

XX 08-NOV-1993; 93US-00148968.

XX 29-DEC-1993; 93US-00175116.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;  
 PI Yang Y, Murrin A, Klein M;

XX WPI; 1995-194089/25.

XX Nucleic acids encoding Haemophilus transferrin receptor - used to develop  
 PT prods for detection and in diagnosis, prevention and treatment of  
 PT Haemophilus infection.

XX Claim 11; Page 72; 231pp; English.

XX AAR77933-969 are predicted antigenic peptides derived from conserved  
 CC regions of the Tbp2 protein from H. influenzae strains Eagan, Minna, DL63  
 CC and non-typable strain PAK12085. The transferrin receptor (TfR) operon  
 CC consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are  
 CC transcribed from a single promoter. H. influenzae TfR is iron- and/or  
 CC haemin-regulated and a putative fur-binding site has been identified  
 CC upstream of Tbp2. Antibodies blocking this binding site may prevent  
 CC bacterial growth. Fragments of the TfR (or its genes) are useful in  
 CC vaccines to provide protection against, e.g. bacterial meningitis. An

CC advantage of using the TfR is that it shares homology with TfR of other  
 CC H. influenzae strains including non-typable strains. According to the  
 CC specification the present sequence shows residues 231-238 of Tbp2 from  
 CC the H. influenzae strain Eagan

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7  
 Db 1 LEGGFYG 7

RESULT 8

AAW46151

ID AAW46151 standard; protein; 8 AA.

AC AAW46151;

DT 05-MAY-1998 (first entry)

XX Predicted antigenic Tbp1 peptide TBP2-25.

XX Transferrin receptor; Haemophilus influenzae type b; iron;  
 KW human transferrin; iron source; antibody; bacterial growth; vaccine;  
 KW immunogenic truncated analogue; antigen; Tbp1; Tbp2.

OS Synthetic.

OS Haemophilus influenzae.

XX WO9640929-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-CA000399.

XX 07-JUN-1995; 95US-00483577.

XX 17-MAY-1996; 96US-00649518.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore SM, Harkness RE, Schryvers AB, Chong P, Gray-Owen S;  
 PI Yang Y, Murrin AD, Klein MH;

XX WPI; 1997-052329/05.

XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used  
 PT to induce protection against disease caused by transferrin producing  
 PT pathogens, or as antigen to detect Haemophilus TfR antibodies.

XX Example 16; Page 71; 228pp; English.

XX AAW46126-62 are predicted antigenic peptides derived from the Tbp2  
 CC protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin  
 CC receptor, of which Tbp1 is also a subunit. The deduced amino acid  
 CC sequences of Tbp1 and Tbp2 were compared, and regions of conservation  
 CC identified. The above peptides are derived from these regions, the  
 CC present peptide being derived from residues 231-238. Iron is an essential  
 CC nutrient for the growth of these bacteria, and they can utilise human  
 CC transferrin as a source of iron. Antibodies which block the access of the  
 CC transferrin receptor to its iron source prevent bacterial growth. The  
 CC transferrin receptor, or fragments, therefore, are good vaccine  
 CC candidates. An immunogenic composition comprising (or encoding) the  
 CC immunogenic truncated analogue can be used to induce protection against a  
 CC disease caused by a bacterial pathogen that produces the transferrin  
 CC receptor. The immunogenic truncated analogue is also useful as an antigen  
 CC in immunoassays for the detection of Haemophilus transferrin receptor  
 CC antibodies, while the nucleic acid molecule can be used as a  
 CC hybridisation probe for the detection of other transferrin receptor genes  
 XX

```

SQ      Sequence 8 AA;
Query Match      100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEGGPGY 7
Db      1 LEGGPGY 7

RESULT 9
AAV51756
ID      AAV51756 standard; protein; 8 AA.
XX
AC      AAV51756;
XX
DT      13-JUN-2000 (first entry)
XX
DE      H. influenzae antigenic Tbp2 peptide TBP2-25.
XX
KW      Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
KW      diagnosis.
XX
OS      Haemophilus influenzae.
XX
PN      US6015688-A.
XX
PD      18-JAN-2000.
XX
PF      07-JUN-1995; 95US-00483577.
XX
PR      08-NOV-1993; 93US-00148968.
PR      29-DEC-1993; 93US-00175116.
PR      08-NOV-1994; 94US-00337483.
XX
PA      (CONN-) CONNAUGHT LAB LTD.
XX
PI      Loosmore S., Harkness R, Schryvers A, Gray-Owen S, Yang Y;
PI      Murdin A, Klein M, Chong P;
XX
DR      WPI; 1997-052329/05.
XX
KW      Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
PT      to induce protection against disease caused by transferrin producing
PT      pathogens, or as antigen to detect Haemophilus Tfr antibodies.
XX
PS      Example 16; Col 39-40; 281pp; English.
XX
CC      This invention describes a novel isolated and purified nucleic acid (I)
CC      encoding an immunogenic, C-terminally truncated analog of one of the
CC      transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
CC      which has antibacterial activity. (I) are used for recombinant production
CC      of truncated Tbp; as probes and primers for detecting, and diagnosing
CC      infection by, Haemophilus, also for isolating similar sequences from
CC      other bacteria; as immunogens for vaccinating against infections caused
CC      by bacteria that produce transferrin receptors, e.g. Haemophilus,
CC      Neisseria or Branhamella. The truncated proteins are useful as immunogens
CC      (as above); for diagnosing infection (as antigens in immunoassays) and
CC      for raising antibodies, used for diagnosis of infections or for passive
CC      immunization. AAV51695-Y51767 represent H. influenzae transferrin
CC      receptor proteins Tbp1 and Tbp2 antigenic peptide fragments
XX
SQ      Sequence 8 AA;
Query Match      100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEGGPGY 7
Db      1 LEGGPGY 7

RESULT 10
AAW54110
ID      AAW54110 standard; peptide; 8 AA.
XX
AC      AAW54110;
XX
DT      20-JUL-1998 (first entry)
XX
DE      Tbp2 antigenic peptide TBP2-25.
XX
KW      tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
KW      passive immunisation; transferrin receptor operon.
XX
OS      Haemophilus influenzae.
XX
PN      US5708149-A.
XX
PD      13-JAN-1998.
XX
PF      07-JUN-1995; 95US-00487890.
XX
PR      08-NOV-1993; 93US-00148968.
PR      29-DEC-1993; 93US-00175116.
PR      08-NOV-1994; 94US-00337483.
XX
PA      (CONN-) CONNAUGHT LAB LTD.
XX
PI      Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;
PI      Murdin A, Schryvers A;
XX
DR      WPI; 1998-100410/09.
XX
KW      Purification of recombinant Haemophilus transferrin-binding protein - by
PT      solubilising inclusion bodies separated from cell lysate.
XX
PS      Example 16/17; Column 37-38; 261pp; English.
XX
CC      Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from
CC      the Tbp2 protein. The Tbp2 protein is one of two proteins with genes
CC      found on the transferrin operon. These peptides can be used along with
CC      the genes, DNA sequences and recombinant proteins for diagnosis.
CC      immunisation and the generation of diagnostic and immunological reagents.
CC      They can also be used to protect from bacteria that produce transferrin
CC      receptor protein
XX
SQ      Sequence 8 AA;
Query Match      100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEGGPGY 7
Db      1 LEGGPGY 7

RESULT 11
AAV80453
ID      AAV80453 standard; peptide; 8 AA.
XX
AC      AAV80453;
XX
DT      06-JUN-2000 (first entry)
XX
DE      H. influenzae transferrin receptor Tbp1 epitope TBP2-25.
XX
KW      Antibacterial; antiinflammatory; auditory; respiratory; antibody;
KW      antiserum; transferrin receptor; immunogen; epitope; otitis media;
KW      bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
XX
OS      Haemophilus influenzae.
XX

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PN US6008326-A.
XX
XX 28-DEC-1999.
XX
XX 07-JUN-1995; 95US-00474671.
XX
XX 08-NOV-1993; 93US-00148968.
XX
XX 29-DEC-1993; 93US-00175116.
XX
XX 08-NOV-1995; 95US-00337483.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
XX Murdin A, Schryvers A;
XX WPI; 2000-096387/08.
XX
XX Antibodies specific for transferrin receptor proteins of Haemophilus
XX influenzae, useful for treating otitis media, epiglottitis, pneumonia and
XX tracheobronchitis.
XX
XX Disclosure; Col 37-38; 252pp; English.
XX
XX The invention relates to novel antibodies (or monospecific antisera)
XX specific for single transferrin receptor proteins (or immunogenic
XX fragment) from strains of Haemophilus influenzae. This sequence
XX corresponds to an epitope from the H. influenzae transferrin receptor
XX protein Tbp2. The antibodies may be used for preventing and treating
XX infections and disorders caused by H. influenzae, including bacterial
XX meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis.
XX The antibodies may also be used to detect the presence of H. influenzae
XX proteins in samples according to standard methodologies (e.g. enzyme
XX linked immunosorbent assay (ELISA)) and hence diagnose infections
XX
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 40; DB 3; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 LEGGFYG 7
Db | | | | |
1 LEGGFYG 7

RESULT 12
AAR77974
ID AAR77974 standard; peptide; 15 AA.
XX
XX AAR77974;
XX
XX 09-OCT-1996 (first entry)
XX
XX H. influenzae TBP2 epitope used to construct pT7TBP2D.
XX
XX Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen; vector;
XX non-typable strain; Haemophilus influenzae; meningitis; poliovirus.
XX
XX Synthetic.
XX
XX WO9513370-A1.
XX
XX 18-MAY-1995.
XX
XX 07-NOV-1994; 94WO-CA000616.
XX
XX 08-NOV-1993; 93US-00148968.
XX
XX 29-DEC-1993; 93US-00175116.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
XX Yang Y, Murdin A, Klein M;

PI
XX
XX WPI; 1995-194089/25.
XX
XX Nucleic acids encoding Haemophilus transferrin receptor - used to develop
XX prods for detection and in diagnosis, prevention and treatment of
XX Haemophilus infection.
XX
XX Example 20; Fig 29; 231pp; English.
XX
XX The transferrin receptor (TfR) operon consists of two genes (Tbp1 and
XX Tbp2) arranged in tandem and which are transcribed from a single
XX promoter. Fragments of the TfR (or its genes) are useful in vaccines to
XX provide protection against, e.g. bacterial meningitis. A cDNA clone
XX (AAQ94452) of the poliovirus type 1, Mahoney strain (PVI-M) genome was
XX cut with Saul and HindIII excising a fragment contg. bases 2754-2786,
XX which encodes AAR77970. (Residues 1095 to amino acid 95 of capsid protein
XX VP1). New hybrid cDNA clones encoding both poliovirus and transferrin
XX receptor amino acid sequences were constructed by replacing the excised
XX fragment with oligonucleotides encoding amino acids from H. influenzae
XX Tbp2 (AAR77971-74). Transfection of Vero cells with the hybrid RNA
XX transcripts produced 4 viable hybrid viruses, designated PVI7BP2A,
XX PVI7BP2B, PVI7BP2C and PVI7BP2D
XX
XX Sequence 15 AA;
XX
XX Query Match 100.0%; Score 40; DB 2; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 LEGGFYG 7
Db | | | | |
7 LEGGFYG 13

RESULT 13
AAY51789
ID AAY51789 standard; protein; 15 AA.
XX
XX AAY51789;
XX
XX 13-JUN-2000 (first entry)
XX
XX H. influenzae transferrin receptor protein fragment #5.
XX
XX Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
XX diagnosis.
XX
XX Haemophilus influenzae.
XX
XX US6015688-A.
XX
XX 18-JAN-2000.
XX
XX 07-JUN-1995; 95US-00483577.
XX
XX 08-NOV-1993; 93US-00148968.
XX
XX 29-DEC-1993; 93US-00175116.
XX
XX 08-NOV-1994; 94US-00337483.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
XX Murdin A, Klein M, Chong P;
XX
XX WPI; 1997-052329/05.
XX
XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
XX to induce protection against disease caused by transferrin producing
XX pathogens, or as antigen to detect Haemophilus TfR antibodies.
XX
XX Disclosure; Col 235-236; 281pp; English.
XX
XX This invention describes a novel isolated and purified nucleic acid (I)
XX

```

CC encoding an immunogenic, C-terminally truncated analog of one of the  
 CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae  
 CC which has antibacterial activity. (1) are used for recombinant production  
 CC of truncated Tbp; as probes and primers for detecting, and diagnosing  
 CC infection by, Haemophilus, also for isolating similar sequences from  
 CC other bacteria; as immunogens for vaccinating against infections caused  
 CC by bacteria that produce transferrin receptors, e.g. Haemophilus,  
 CC Neisseria or Branhamella. The truncated proteins are useful as immunogens  
 CC (as above); for diagnosing infection (as antigens in immunoassays) and  
 CC for raising antibodies, used for diagnosis of infections or for passive  
 CC immunization. This sequence represents a fragment of a H. influenzae  
 CC transferrin receptor protein  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 40; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEGGFGY 7  
 |||||  
 Db 7 LEGGFGY 13

RESULT 14  
 AAW54133  
 ID AAW54133 standard; peptide; 15 AA.  
 XX  
 AC AAW54133;

DT 20-JUL-1998 (first entry)

DE Poliovirus plasmid PV1TBP2 encoded peptide.

KE Transferrin receptor; antigen; virus; prevention; pathogens.

OS Synthetic.

OS Poliovirus.  
 OS Haemophilus Influenzae.

XX US5708149-A.

PD 13-JAN-1998.

PF 07-JUN-1995; 95US-00487890.

PR 08-NOV-1993; 93US-00148968.

PR 29-DEC-1993; 93US-00175116.

PR 08-NOV-1994; 94US-00337483.

XX (CONN-) CONNAUGHT LAB LTD.

XX Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;  
 PI Murdin A, Schryvers A;

XX WPI; 1998-100410/09.

XX Purification of recombinant Haemophilus transferrin-binding protein - by  
 PT solubilising inclusion bodies separated from cell lysate.

PS Example 20; Fig 29; 261pp; English.

XX Peptides (AAW54129-W54133) are encoded by plasmids encoding a chimeric  
 CC poliovirus expressing an epitope LEGGFGY. The epitope is derived from  
 CC the transferrin receptor protein that is conserved among bacteria that  
 CC produce transferrin receptor protein. These viruses expressed the epitope  
 CC sequence in an antigenically recognisable form. Viruses based upon  
 CC expressed recombinant transferrin receptor protein can be used for the  
 CC prevention of diseases caused by bacterial pathogens that produce  
 CC transferrin receptor  
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 40; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEGGFGY 7  
 |||||  
 Db 7 LEGGFGY 13

RESULT 15  
 AAY80391  
 ID AAY80391 standard; protein; 15 AA.  
 XX  
 AC AAY80391;

DT 06-JUN-2000 (first entry)

DE H. influenzae transferrin receptor protein epitope TBP2D.

XX Antibacterial; antiinflammatory; auditory; respiratory; antibody; primer;  
 KW antiserum; transferrin receptor; immunogen; epitope; otitis media; PCR;  
 KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ss.

OS Haemophilus influenzae.

XX US6008326-A.

PD 28-DEC-1999.

PF 07-JUN-1995; 95US-00474671.

PR 08-NOV-1993; 93US-00148968.

PR 29-DEC-1993; 93US-00175116.

PR 08-NOV-1995; 95US-00337483.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;  
 PI Murdin A, Schryvers A;

XX WPI; 2000-096387/08.

XX Antibodies specific for transferrin receptor proteins of Haemophilus  
 PT Influenzae, useful for treating otitis media, epiglottitis, pneumonia and  
 PT tracheobronchitis.

XX Example 20; Fig 29; 252pp; English.

XX The invention relates to novel antibodies (or monospecific antisera)  
 CC specific for single transferrin receptor proteins (or immunogenic  
 CC fragment) from strains of Haemophilus influenzae. The antibodies can be  
 CC generated by expressing transferrin receptor epitope on the surface of a  
 CC vector protein. In an example, the vector is poliovirus and the epitopes  
 CC are inserted into the capsid protein VP1. This sequence corresponds to  
 CC the transferrin receptor epitope TBP2D which is used to replace amino  
 CC acids 95-102 of the poliovirus VP1 capsid protein (AAY80387). The  
 CC antibodies may be used for preventing and treating infections and  
 CC disorders caused by H. influenzae, including bacterial meningitis, otitis  
 CC media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may  
 CC also be used to detect the presence of H. influenzae proteins in samples  
 CC according to standard methodologies (e.g. enzyme linked immunosorbent  
 CC assay (ELISA)) and hence diagnose infections

SQ Sequence 15 AA;

Query Match 100.0%; Score 40; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEGGFGY 7  
 |||||  
 Db 7 LEGGFGY 13

Search completed: November 9, 2005, 19:22:43  
Job time : 32.6296 secs

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